

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/537,143
Source: PAT
Date Processed by STIC: 3/2/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/02/2006

PATENT APPLICATION: US/10/537,143

TIME: 10:31:42

Input Set : E:\9632082999.txt

Output Set: N:\CRF4\03022006\J537143.raw

3 <110> APPLICANT: Franciso, Joseph
 4 McDonagh, Charlotte
 6 <120> TITLE OF INVENTION: MODIFIED L49-sFv EXHIBITING INCREASED STABILITY AND METHODS
 OF USE
 7 THEREOF
 9 <130> FILE REFERENCE: 9632-082-999
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,143
 C--> 12 <141> CURRENT FILING DATE: 2005-06-01
 14 <160> NUMBER OF SEQ ID NOS: 23
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 753
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (1)..(753)
 27 <400> SEQUENCE: 1
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 29 Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser
 30 1 5 10 15
 31 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt 96
 32 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser
 33 20 25 30
 34 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat 144
 35 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr
 36 35 40 45
 37 atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc 192
 38 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
 39 50 55 60
 40 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac 240
 41 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
 42 65 70 75 80
 43 ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt 288
 44 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
 45 85 90 95
 46 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa 336
 47 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
 48 100 105 110
 49 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa 384
 50 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
 51 115 120 125
 52 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa 432
 53 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln

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54      130      135      140
55 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct      480
56 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
57 145      150      155      160
58 tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta      528
59 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu
60      165      170      175
61 cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc tac      576
62 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
63      180      185      190
64 aga gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt      624
65 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
66      195      200      205
67 gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag      672
68 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
69      210      215      220
70 gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt cct ccg acg      720
71 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr
72 225      230      235      240
73 ttc ggt gga ggc acc aag ctg gaa atc aaa cgg      753
74 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
75      245      250
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78 <211> LENGTH: 251
79 <212> TYPE: PRT
80 <213> ORGANISM: Homo sapiens
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86 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser
87      20      25      30
89 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr
90      35      40      45
92 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
93      50      55      60
95 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
96 65      70      75      80
98 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
99      85      90      95
101 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
102      100      105      110
104 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
105      115      120      125
107 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln
108      130      135      140
110 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
111 145      150      155      160
113 Cys Arg Ala Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu
114      165      170      175

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116 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
117      180      185      190
119 Arg Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
120      195      200      205
122 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
123      210      215      220
125 Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Pro Thr
126 225      230      235      240
128 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
129      245      250
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 1839
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (1)..(1839)
140 <400> SEQUENCE: 3
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142 Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser
143 1      5      10      15
144 cag act ctg tcc ctc acc tgt tct gtc act ggc gac tcc atc acc agt      96
145 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser
146      20      25      30
147 ggt tac tgg aac tgg atc cgg aag ttc cca ggg aat aaa ctt gaa tat      144
148 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr
149      35      40      45
150 atg ggt tac ata agc gac agt ggt atc act tac tac aat cca tct ctc      192
151 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu
152      50      55      60
153 aaa agt cgc att tcc atc act cga gac aca tcc aag aac caa tac tac      240
154 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Tyr
155 65      70      75      80
156 ctc cag ttg aat ttt gtg act gct gag gac aca gcc aca tat aac tgt      288
157 Leu Gln Leu Asn Phe Val Thr Ala Glu Asp Thr Ala Thr Tyr Asn Cys
158      85      90      95
159 gca aga agg act ctg gct act tac tat gct atg gac tac tgg ggt caa      336
160 Ala Arg Arg Thr Leu Ala Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
161      100      105      110
162 gga acc tct gtc acc gtc tcc tca ggc tcg acg tcc ggc tct ggc aaa      384
163 Gly Thr Ser Val Thr Val Ser Ser Gly Ser Thr Ser Gly Ser Gly Lys
164      115      120      125
165 ccg ggc tct ggc gaa ggc tct acc aag ggc gat ttt gtg atg acc caa      432
166 Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Asp Phe Val Met Thr Gln
167      130      135      140
168 act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct      480
169 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
170 145      150      155      160
171 tgc agg gct agt cag agc ctt gta cac agt aat gga aac acc tat tta      528

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172	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	
173					165					170					175		
174	cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	576
175	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	
176					180					185					190		
177	aga	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	624
178	Arg	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	
179					195					200					205		
180	gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	672
181	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	
182			210						215						220		
183	gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	cct	ccg	acg	720
184	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Pro	Thr	
185	225						230					235				240	
186	ttc	ggt	gga	ggc	acc	aag	ctg	gaa	atc	aaa	cgg	acg	cca	gtg	tca	gaa	768
187	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Pro	Val	Ser	Glu	
188						245					250					255	
189	aaa	cag	ctg	gcg	gag	gtg	gtc	gcg	aat	acg	att	acc	ccg	ctg	atg	aaa	816
190	Lys	Gln	Leu	Ala	Glu	Val	Val	Ala	Asn	Thr	Ile	Thr	Pro	Leu	Met	Lys	
191					260					265						270	
192	gcc	cag	tct	gtt	cca	ggc	atg	gcg	gtg	gcc	gtt	att	tat	cag	gga	aaa	864
193	Ala	Gln	Ser	Val	Pro	Gly	Met	Ala	Val	Ala	Val	Ile	Tyr	Gln	Gly	Lys	
194					275											285	
195	ccg	cac	tat	tac	aca	ttt	ggc	aag	gcc	gat	atc	gcg	gcg	aat	aaa	ccc	912
196	Pro	His	Tyr	Tyr	Thr	Phe	Gly	Lys	Ala	Asp	Ile	Ala	Ala	Asn	Lys	Pro	
197								295								300	
198	gtt	acg	cct	cag	acc	ctg	ttc	gag	ctg	ggt	tct	ata	agt	aaa	acc	ttc	960
199	Val	Thr	Pro	Gln	Thr	Leu	Phe	Glu	Leu	Gly	Ser	Ile	Ser	Lys	Thr	Phe	
200	305						310									320	
201	acc	ggc	gtt	tta	ggt	ggg	gat	gcc	att	gct	cgc	ggt	gaa	att	tgc	ctg	1008
202	Thr	Gly	Val	Leu	Gly	Asp	Ala	Ile	Ala	Arg	Gly	Glu	Ile	Ser	Leu		
203							325				330					335	
204	gac	gat	gcg	gtg	acc	aga	tac	tgg	cca	cag	ctg	acg	ggc	aag	cag	tgg	1056
205	Asp	Asp	Ala	Val	Thr	Arg	Tyr	Trp	Pro	Gln	Leu	Thr	Gly	Lys	Gln	Trp	
206							340				345					350	
207	cag	ggt	att	cgt	atg	ctg	gat	ctc	gcc	acc	tac	acc	gct	ggc	ggc	ctg	1104
208	Gln	Gly	Ile	Arg	Met	Leu	Asp	Leu	Ala	Thr	Tyr	Thr	Ala	Gly	Gly	Leu	
209																365	
210	ccg	cta	cag	gta	ccg	gat	gag	gtc	acg	gat	aac	gcc	tcc	ctg	ctg	cgc	1152
211	Pro	Leu	Gln	Val	Pro	Asp	Glu	Val	Thr	Asp	Asn	Ala	Ser	Leu	Leu	Arg	
212																380	
213	ttt	tat	caa	aac	tgg	cag	ccg	cag	tgg	aag	cct	ggc	aca	acg	cgt	ctt	1200
214	Phe	Tyr	Gln	Asn	Trp	Gln	Pro	Gln	Trp	Lys	Pro	Gly	Thr	Thr	Arg	Leu	
215	385						390					395				400	
216	tac	gcc	aac	gcc	agc	atc	ggt	ctt	ttt	ggt	gcg	ctg	gcg	gtc	aaa	cct	1248
217	Tyr	Ala	Asn	Ala	Ser	Ile	Gly	Leu	Phe	Gly	Ala	Leu	Ala	Val	Lys	Pro	
218							405									415	
219	tct	ggc	atg	ccc	tat	gag	cag	gcc	atg	acg	acg	cgg	gtc	ctt	aag	ccg	1296
220	Ser	Gly	Met	Pro	Tyr	Glu	Gln	Ala	Met	Thr	Thr	Arg	Val	Leu	Lys	Pro	

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221          420          425          430
222 ctc aag ctg gac cat acc tgg att aac gtg ccg aaa gcg gaa gag gcg      1344
223 Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala
224          435          440          445
225 cat tac gcc tgg ggc tat cgt gac ggt aaa gcg gtg cgc gtt tcg ccg      1392
226 His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro
227          450          455          460
228 ggt atg ctg gat gca caa gcc tat ggc gtg aaa acc aac gtg cag gat      1440
229 Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp
230 465          470          475          480
231 atg gcg aac tgg gtc atg gca aac atg gcg ccg gag aac gtt gct gat      1488
232 Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp
233          485          490          495
234 gcc tca ctt aag cag ggc atc gcg ctg gcg cag tcg cgc tac tgg cgt      1536
235 Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg
236          500          505          510
237 atc ggg tca atg tat cag ggt ctg ggc tgg gag atg ctc aac tgg ccc      1584
238 Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro
239          515          520          525
240 gtg gag gcc aac acg gtg gtc gag acg agt ttt ggt aat gta gca ctg      1632
241 Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu
242          530          535          540
243 gcg ccg ttg ccc gtg gca gaa gtg aat cca ccg gct ccc ccg gtc aaa      1680
244 Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys
245 545          550          555          560
246 gcg tcc tgg gtc cat aaa acg ggc tct act ggc ggg ttt ggc agc tac      1728
247 Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr
248          565          570          575
249 gtg gcc ttt att cct gaa aag cag atc ggt att gtg atg ctc gcg aat      1776
250 Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn
251          580          585          590
252 aca agc tat ccg aac ccg gca cgc gtt gag gcg gca tac cat atc ctc      1824
253 Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu
254          595          600          605
255 gag gcg cta cag tag      1839
256 Glu Ala Leu Gln
257          610
259 <210> SEQ ID NO: 4
260 <211> LENGTH: 612
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 4
265 Met Glu Val Gln Leu Gln Glu Ser Gly Pro Ser Leu Val Lys Pro Ser
266 1          5          10          15
268 Gln Thr Leu Ser Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser
269          20          25          30
271 Gly Tyr Trp Asn Trp Ile Arg Lys Phe Pro Gly Asn Lys Leu Glu Tyr
272          35          40          45
274 Met Gly Tyr Ile Ser Asp Ser Gly Ile Thr Tyr Tyr Asn Pro Ser Leu

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : E:\9632082999.txt

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23

VERIFICATION SUMMARY

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Input Set : E:\9632082999.txt

Output Set: N:\CRF4\03022006\J537143.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date